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## Details



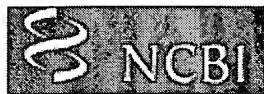
## Links

### MAP DATA

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Mar 17 2003 10:55:57



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☐ 1: AC024008. Homo sapiens chro...[gi:7249353]

Links

LOCUS AC024008 164352 bp DNA linear HTG 16-MAR-2000  
DEFINITION Homo sapiens chromosome 1 clone RP11-158A1 map 1, WORKING DRAFT  
SEQUENCE, 24 unordered pieces.  
ACCESSION AC024008  
VERSION AC024008.2 GI:7249353  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 164352)  
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
TITLE Homo sapiens chromosome 1, clone RP11-158A1  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 164352)  
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L.,  
Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,  
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Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and  
Zody,M.  
TITLE Direct Submission  
JOURNAL Submitted (20-FEB-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
COMMENT On Mar 16, 2000 this sequence version replaced gi:7008913.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
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Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L7214  
Center clone name: 158\_A\_1  
----- Summary Statistics  
Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 144810 bases at least Q40  
Consensus quality: 154190 bases at least Q30  
Consensus quality: 158804 bases at least Q20  
Insert size: 170000; agarose-fp  
Insert size: 162052; sum-of-contigs  
Quality coverage: 3.5 in Q20 bases; agarose-fp  
Quality coverage: 3.6 in Q20 bases; sum-of-contigs

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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 24 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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\*       1219       2378: contig of 1160 bp in length  
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\*       2479       4229: contig of 1751 bp in length  
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\*       4330       5720: contig of 1391 bp in length  
\*       5721       5820: gap of 100 bp  
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## Identification and Categorization of Inducible Mast Cell Genes in a Subtraction Library

Jeong-Je Cho,\* Harissios Vliagoftis,† Vanitcha Rumsaeng,† Dean D. Metcalfe,† and Chad K. Oh\*<sup>1</sup>

\*Division of Allergy and Immunology, Department of Pediatrics, Harbor-UCLA Medical Center, Torrance, California 90502; and †Laboratory of Allergic Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland 20892-1881

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Mast cells play an important role in allergic inflammation by releasing inducible proinflammatory cytokines. While many inducible genes have been identified, we hypothesized that a significant number remain to be identified. We thus constructed an activation-specific mast cell subtraction library to establish a profile of induced genes in mast cells following allergic stimulation. To date, we have sequenced 150 cDNA clones. Among them, we have isolated 22 known genes whose expression has not been reported in mast cells, and an additional 26 cDNA clones which do not have significant homology to known genes in the Genbank database. We next selected 10 cDNA clones with strong signals by differential plaque hybridization. Of these cDNA clones, five genes were induced in mast cells upon FcεRI-mediated stimulation. They are cofilin, annexinVI, interferon (IFN)-β, serglycin, and a novel inducible mast cell (IMC) gene, IMC-415. Characterization and relevant studies of this novel gene and other inducible known genes in mast cells will provide insight into the functions of mast cells in mammalian biology. © 1998 Academic Press

The mast cell is an essential effector cell in allergic inflammation through its capacity to respond to IgE-dependent activation with release of both preformed and newly generated mediators (1). Mast cells also participate in the modulation of physiologic processes, including delayed type hypersensitivity reactions (2), fibrosis (3), autoimmune processes (4), neoplasia (5), inflammation in the rheumatoid synovium (6), and in inflammatory bowel diseases (7).

In spite of potent biological activities, there appears much to be learned about the expression and function of inducible mast cell genes and proteins in response

to allergic stimulation. We thus constructed a cDNA subtraction library which was enriched by removing mRNA common to resting cells and cells stimulated by PMA and the ionophore A23187. Subsequently, isolated genes were tested for inducibility upon FcεRI-mediated stimulation. Similar approaches have been used to identify new or novel genes in macrophages (8), lymphocytes (9), and nerve cells (10).

This is the first report of a profile of genes expressed in mast cells and 5 inducible genes including IMC-415 upon stimulation.

### MATERIALS AND METHODS

**Cells.** The interleukin-3 (IL-3)-independent cloned mast cell line CLMC/C57.1 (kind gift of S. Galli, Harvard Medical School, Boston, MA) and IL-3-dependent primary bone marrow cultured mast cells (BMCMC) were maintained as described (11).

**Stimulation conditions.** For FcεRI-dependent activation, mast cells were adjusted to a density of  $1 \times 10^6$  cells/ml in complete Dulbecco's Modified Eagle Medium (DMEM), 0.5 mg/ml of IgE anti-DNP was added, and the cells were incubated at 37°C for 60 min.

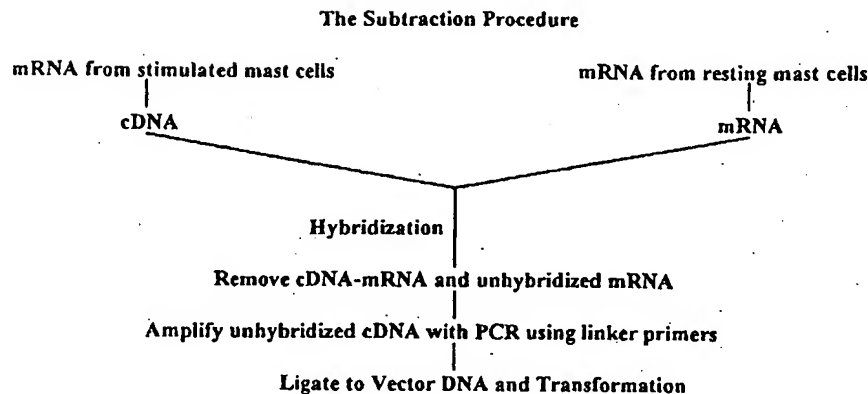
Cells were then centrifuged at  $400 \times g$  at 4°C for 10 min and the cell pellets resuspended in fresh media. Antigen-mediated degranulation was performed by addition of DNP<sub>30-40</sub>-human serum albumin (HSA) (Sigma Chemical Co., St. Louis, MO) to a final concentration at 40 ng/ml. Where indicated, PMA (Sigma) was added at 50 ng/ml, A23187 (Sigma) at 0.5 mM, ionomycin (Sigma) at 1 mM, and recombinant murine stem cell factor (rmSCF) at 5 or 50 ng/ml. The reaction was terminated at a specific time point.

**cDNA probes for Northern Blot analysis.** cDNA fragments were labeled by random hexamer priming using primers and protocols suggested by the manufacturers (Stratagene) (12).

**Northern Blot analysis.** Twenty μg of whole cell RNA was isolated and then subjected to electrophoresis in 1.5% agarose-formaldehyde gels and transferred to nylon-reinforced nitrocellulose membranes (MSI, Westboro, MA) (13). Prehybridizations were performed at 37°C for 30 min. Hybridizations were performed at 37-42°C for 18-24 h in 50% formamide, 5 x Denhardt's solution, 0.55 M NaCl, 0.09 M NaPO<sub>4</sub> (pH 7.0), 0.4 mM Na<sub>2</sub>EDTA, 0.09 M sodium pyrophosphate, 0.5% SDS, and 100 μg/ml denatured salmon sperm DNA.

**Construction of the Subtractive cDNA Library.** The subtraction library was constructed as described with minor modifications (14).

<sup>1</sup> To whom correspondence should be addressed. Fax: (310) 212-7440.



**FIG. 1.** Schematic illustration of the construction of a subtractive cDNA library. The subtractive hybridization employed oligo (dT)30-Latex.

a. Subtractive hybridization. Twenty  $\mu$ l of sense-strand DNA prepared from activated cells was hybridized with cDNA-Oligotex particles from resting cells in the hybridization buffer (50 mM Tris, pH 7.5, 5 mM EDTA, 500 mM NaCl, 0.5% SDS) at 55°C for 50 min. This subtractive hybridization step was repeated four times in total.

b. cDNA Cloning in  $\lambda$ Phage Vectors - Amplified cDNA was digested with *Eco*RI and *Xho*I, ligated with Uni Zap XR Vector, and in vitro packaging performed using packaging extract (Epicenter Technologies, Madison, WI).

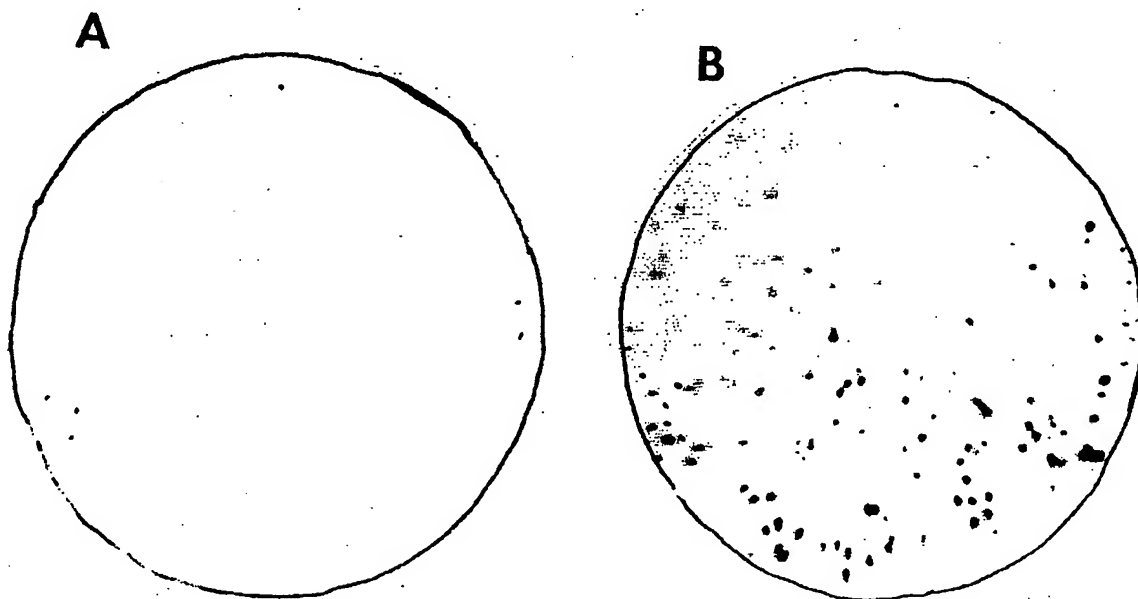
c. cDNA library screening. Five hundred thousand clones were screened with  $^{32}$ P-labeled cDNA probe from subtracted cDNA. Positive plaques were picked and rescreened as described above except that the number of plaques per plate were decreased to 500-1000. After tertiary screening, positive plaques were picked and resuspended in 1 ml of SM medium (15). Final screening was performed

by dot blot analysis of the positive clones using probes from activated and resting cells. The plaques were spotted in triplicate and hybridized with these probes separately.

## RESULTS

### *Construction and Screening of the cDNA Library*

To identify genes induced during mast cell activation, a subtractive cDNA library was constructed with mRNA of a murine mast cell line, C1.MC/C57.1. The mRNA was enriched by removing mRNA common to resting cells and cells stimulated with PMA and



**FIG. 2.** Differential plaque hybridization. The subtractive cDNA library was screened for clones preferentially expressed in stimulated mast cells by successive differential plaque hybridizations. The positive clones at the second hybridization were spotted onto the bacterial lawn in duplicate. The plaque hybridization was then repeated with  $^{32}$ P-labeled cDNA probes prepared from either resting (A) or stimulated (B) mast cells.

M 1 2 3 4 5 6 7 8 9 10 11 12 13 14

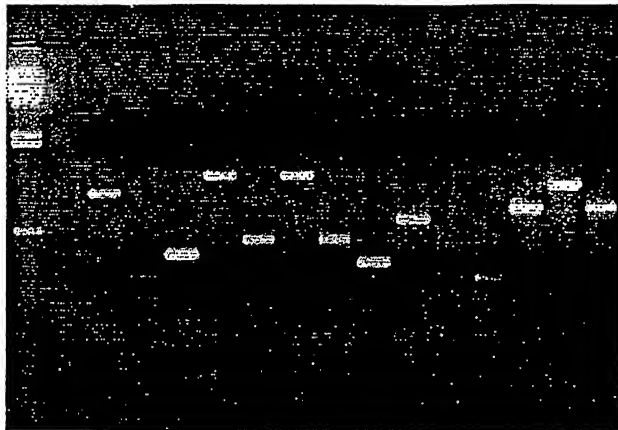


FIG. 3. Sizes of cDNA inserts. The plasmid, pBluescript carrying the cDNA insert, was generated from  $\lambda$ ZapII recombinants by co-transfection of *E. coli* XL1-blue with the f1 helper phage. The cell lysates and the plasmid DNA were prepared by heating the infected cells at 70°C for 15 min. *E. coli* XL1-blue was transfected with the lysates and the plasmid DNA were prepared from ampicillin resistant transformants. The DNA were PCR-amplified with T3 and T7 primers and electrophoresed in 1% agarose gels. The DNA fragments were stained with ethidium bromide.  $\lambda$  HindIII was used as a molecular marker.

A23187 (Fig. 1) (14). The mast cell line was used for its homogeneity and to avoid contamination with other cells. A combination of PMA and A23187 was used in order to achieve maximum stimulation of mast cells. The library was screened for phage colonies containing activation specific sequences by differential plaque hybridization with cDNAs probe prepared from resting and activated mast cells. Greater than 90% of the colonies showed preferential hybridization to the cDNA probe from activated mast cells (Fig. 2). To estimate average lengths of cDNA inserts, plasmid DNAs were excised from 14 randomly selected recombinant phages as described in Materials and Methods. The DNAs were PCR-amplified with T3 and T7 primers and analyzed on 1% agarose gels. The lengths of cDNA inserts ranged from 0.2 to 2 kb (Fig. 3).

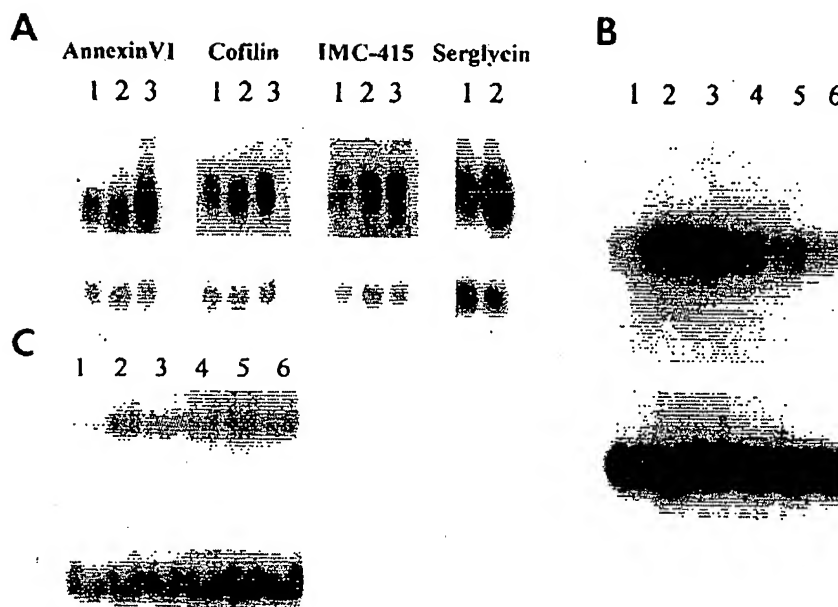
#### DNA Sequence Analysis

One hundred and fifty colonies with insert sizes 200 bp or larger were selected and sequenced on both strands. Nucleic acid sequences obtained from these clones were compared to known sequences using the BLAST network of the NCBI (Table I). Cytokine genes have been isolated from mast cells (16). However, there is no profile of genes expressed in mast cells. In other

TABLE I  
cDNA Clones Isolated from the Mast Cell Subtraction Library<sup>a</sup>

| Known genes                               |   | Unknown genes |     |
|---|---|---------------|-----|
| Previously identified cDNAs in mast cells | cDNAs not previously identified in mast cells                           |               |     |
| 2 Lymphotoxin                             | 12 IFN-beta   | 22            | 671 |
| 3 MIP-1 alpha                             | 21 G-protein-beta subunit   | 96            | 713 |
| 13 PCNA                                   | 23 Connexin 43  | 105           | 721 |
| 16 Ubiquitin                              | 27 Mbh (myc basic motif homolog)-1                                      | 112           |     |
| 20 MIP-1 beta                             | 30 Sec 61   | 127           |     |
| 54 TCA3                                   | 104 RNA helicase  | 143           |     |
| 95 MMCP 5 (chymase 1)                     | 107 Gamma-actin   | 154           |     |
| 115 MMCP 1                                | 142 Retinoic acid inducible E3  | 160           |     |
| 116 Cathepsin                             | 163 A-X actin   | 201           |     |
| 123 Glyceraldehyde-3-phosphate            | 221 Endogenous murine leukemia proviral flanking region & Insertion DNA | 230           |     |
| 134 Aldolase A                            | 226 TRAP (translocin associated protein)                                | 241           |     |
| 663 Hexokinase                            | 248 Beta-galactoside binding protein                                    | 253           |     |
| 666 Tryptophan hydroxylase                | 254 p24.6 protein   | 259           |     |
| 686 c-raf                                 | 303 Alpha-tubulin isotype   | 267           |     |
| 699 Mast cell CPA                         | 311 Rab 7   | 346           |     |
| 714 Phosphoglycerate kinase               | 541 Teg 23  | 415           |     |
| 717 Serglycin                             | 607 Cofilin   | 418           |     |
|   | 633 Annexin VI  | 432           |     |
|   | 650 PR264 (SC35)  | 562           |     |
|   | 672 TCP-1 beta subunit  | 591           |     |
|   | 679 MPR 46 mRNA   | 596           |     |
|   | 680 Thymosin beta-4   | 597           |     |
|   |   | 667           |     |

<sup>a</sup> Numbers represent the specific cDNA clones isolated from subtraction library. Genes encoding mitochondrial DNA, ribosomal protein, and clones with unclear sequences are not included. When multiple clones represent the same gene, only one clone is shown.



**FIG. 4.** (A). Expression levels of subtractive cDNA clones in resting and stimulated cells. Twenty  $\mu$ g of total RNA was subjected to Northern blot analysis. **Upper panel:**  $^{32}$ P-labeled probes were prepared from cDNA encoding annexinVI, cofilin, IMC-415 and mRNA. RNA was loaded from resting mast cells (lane 1) or mast cells treated with PMA and A23187 (lane 2), or following Fc $\epsilon$ RI crosslinking (lane 3). **Lower panel:** Corresponding  $\beta$ -actin. (B). Kinetics of the IFN- $\beta$  mRNA induction in mast cells. **Upper panel:**  $^{32}$ P-labeled probes were prepared from cDNA encoding IFN- $\beta$  mRNA. RNA was loaded from resting mast cells (lane 1) or mast cells treated with PMA and A23187 for 1 h (lane 2), 3 h (lane 3), 5 h (lane 4), or following Fc $\epsilon$ RI crosslinking for 3 h (lane 5), 5 h (lane 6). **Lower panel:** Corresponding  $\beta$ -actin. (C). Effect of SCF on the expression of serglycin mRNA. **Upper panel:** BMCMC were either left untreated (lane 1); or treated with PMA (lane 2), A23187 (lane 3), 5 ng/ml (lane 4) or 50 ng/ml (lane 5) of rmSCF for 4 h, or Fc $\epsilon$ RI crosslinking for 3 h (lane 6) before preparation of total RNA and analysis of serglycin mRNA levels by Northern hybridization. **Lower panel:** Corresponding  $\beta$ -actin.

cell types, subtracted libraries helped identify new genes and give indications about the function of the cell type (8). To date, we have thus isolated 48 expressed genes. Twenty two genes have not been reported previously as being expressed in mast cells. The other 26 cDNA clones do not have significant homology to known genes in the Genbank database (Table I). Chemokines were the major cytokines induced in activated mast cells, as has been reported in an activated macrophage cDNA library (17). Other mast cell cytokines such as TNF- $\alpha$ , interleukin-4 (IL-4) and IL-6 were not found in our activation-specific library and a mast cell library constructed without activation (18). These results suggest that mast cells may be an important source of chemokines during inflammatory reactions.

#### *Isolation of Inducible cDNA Clones from Stimulated Mast Cells*

From the genes in Table I, we selected 10 cDNA clones with strong signals by differential plaque hybridization. Of these cDNA clones, five genes were induced in mast cells upon Fc $\epsilon$ RI-mediated stimulation. They are cofilin, annexinVI, interferon (IFN)- $\beta$ , serglycin, and IMC-415 (Fig. 4). Messages were upregu-

lated following stimulation of mast cells. Rapid induction of cofilin, annexinVI, serglycin, and IMC-415 mRNA expression upon stimulation by Fc $\epsilon$ RI aggregation was similar to the induction pattern of most proinflammatory cytokines, suggesting that these genes may be important in mast cell function.

Cofilin (Table I, Fig. 4A) is a mediator of costimulatory signals via the accessory receptors CD2, CD4, and CD8 (19), suggesting that cofilin may have a role in mediating Fc $\epsilon$ RI-mediated stimulatory signals in mast cells. Similarly, it has been shown that annexinVI is phosphorylated in vitro by p56lck in a human T cell line (Jurkat) (20). T cell activation causes association of p56lck phosphoprotein with annexinVI, suggesting that annexinVI may also participate in signal transduction in mast cells upon stimulation.

IFN- $\beta$  is a known proinflammatory cytokine in other cell types and the kinetics have been well described. In order to examine the kinetics of IFN- $\beta$  message induction in mast cells in comparison to other cell types, a more detailed analysis was performed. IFN- $\beta$  message was induced by 1 h in mast cells after treatment with PMA and A23187, maintained a high level at 3 h, and reduced significantly by 5 h (Fig. 4B). A pattern seen in other cell types where IFN- $\beta$  is believed to play a



role in inflammation, IFN- $\beta$  message was induced similarly in mast cells stimulated by Fc $\epsilon$ RI aggregation.

Serglycin mRNA was induced by multiple signals, including rmSCF, in a dose responsive manner (Fig. 4C). Participation of proteoglycan (PG) has been implicated in the growth and differentiation of hematopoietic cells. Several reports have shown that PGs are extruded from mast cells after activation (21). rmSCF acts as a competence factor for mast cell progenitor growth and profoundly influences certain stages of mast cell differentiation (22). Here, we report that the levels of serglycin mRNA were increased following treatment with rmSCF as well as IgE receptor cross-linking (Fig. 4C). This observation is consistent with the need for activated mast cells to re-synthesize extruded components to restore (23).


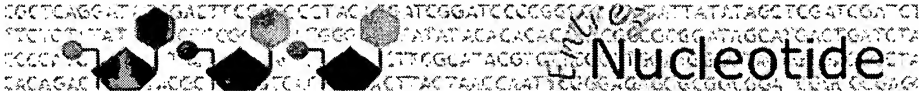
In summary, we have sequenced 150 cDNA clones. Among them, twenty two genes which have not been reported in mast cells and the other 26 cDNA clones which do not have significant homology to known genes in the Genbank database have been isolated. This is the first reported profile of genes expressed and induced in activated mast cells. In the profile of induced genes in these cells, chemokines are especially prominent. We subsequently identified and partially characterized 5 inducible mast cell genes including a novel gene, IMC-415. Protein expression of the IMC-415 cDNA and antibody production may provide information about the biologic function. Results from this study provide insight into the biologic functions of mast cells in inflammation.

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Revised: July 5, 2002.

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Mar 17 2003 10:55:57

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 RL Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan  
 RL (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/,  
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 CC synthesized using specific 5' and 3' primers and amplified  
 CC by PCR. The PCR product was digested with SfiI and size selection  
 CC was performed to exclude fragments <1.5kb. The SfiI-digested  
 CC PCR product was cloned into distinct DraIII sites of pME18S-FL3.  
 CC XhoI sites just outside the DraIII sites can be used to  
 CC isolate the cDNA insert. Libraries were constructed by  
 CC oligo-capping method  
 CC (Sugano et al., , Institute of Medical Science, University of  
 CC Tokyo).  
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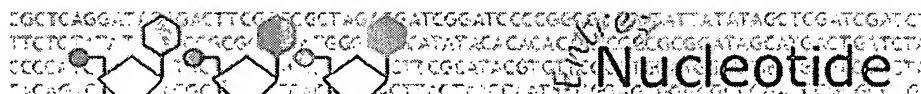
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☐ 1: AK021475. Homo sapiens cDNA...[gi:10432667]

Links

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 AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,  
 Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,  
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 Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.  
 TITLE NEDO human cDNA sequencing project  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 2096)  
 AUTHORS Isogai,T. and Otsuki,T.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,  
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
 COMMENT NEDO human cDNA sequencing project supported by Ministry of  
 International Trade and Industry of Japan; cDNA full insert  
 sequencing: Research Association for Biotechnology; cDNA library  
 construction, 5'- & 3'-end one pass sequencing and clone selection:  
 Helix Research Institute (supported by Japan Key Technology Center  
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☐ 1: AL365261[gi:9931838] This record was replaced or removed. See [revision history](#) for details.

LOCUS AL365261 137865 bp DNA linear HTG 20-JAN-2001

DEFINITION Homo sapiens chromosome 1 clone RP11-6B6, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 27 unordered pieces.

ACCESSION AL365261

VERSION AL365261.6 GI:9931838

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 137865)

AUTHORS Plumb,B.

TITLE Direct Submission

JOURNAL Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Aug 28, 2000 this sequence version replaced gi:9930982.

----- Genome Center

Center: Sanger Centre

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: bA6B6

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 127170 bases at least Q40

Consensus quality: 130854 bases at least Q30

Consensus quality: 132943 bases at least Q20

Insert size: 135265; sum-of-contigs

Insert size: 174864; 13.2% error; agarose-fp

Quality coverage: 3.51x in Q20 bases; sum-of-contigs Quality

coverage: 2.93x in Q20 bases; agarose-fp

-----

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 27 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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 \* 9597 9696: gap of 100 bp  
 \* 9697 13471: contig of 3775 bp in length  
 \* 13472 13571: gap of 100 bp  
 \* 13572 17130: contig of 3559 bp in length  
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 \* 17231 23189: contig of 5959 bp in length

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 XX  
 SV BF242113.1  
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
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 RL Unpublished.  
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 DR RZPD; IMAGp958A01993; IMAGp958A01993.  
 DR UNILIB; 5948; 5948.  
 XX  
 CC Contact: Robert Strausberg, Ph.D.  
 CC Tel: (301) 496-1550  
 CC Email: Robert\_Strausberg@nih.gov  
 CC Tissue Procurement: ATCC  
 CC cDNA Library Preparation: CLONETECH Laboratories, Inc.  
 CC cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 CC DNA Sequencing by: Incyte Genomics, Inc.  
 CC Clone distribution: MGC clone distribution information can be  
 CC found through the I.M.A.G.E. Consortium/LLNL at:  
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 FT ); Double-stranded cDNA was prepared from cell line RNA. 5'  
 FT and 3' adaptors were used in cloning as follows: 5' adaptor  
 FT sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:  
 FT 5'-ATTCTAGAGGCCGAGGCCGCCGACATG-dT(30)BN-3' (where B = A, C,  
 FT or G and N = A, C, G, or T). Average insert size 1.65 kb  
 FT (range 0.9-4.0 kb). 14/15 colonies contained inserts by  
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 FT was constructed by Clontech Laboratories (Palo Alto, CA)."  
 FT /organism="Homo sapiens"  
 FT /clone="IMAGE:4109064"  
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 FT /tissue\_type="from acute myelogenous leukemia"  
 FT /lab\_host="DH10B (T1 phage-resistant)"  
 XX  
 SQ Sequence 527 BP; 183 A; 109 C; 119 G; 115 T; 1 other;

17.9.2002 10:24

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